

FIGURE 1

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graph TD
    201([START]) --> 202[STORE NEW SEQUENCE TO A MEMORY]
    202 --> 204[OPEN DATABASE OF SEQUENCES]
    204 --> 206[READ FIRST SEQUENCE IN DATABASE]
    206 --> 210[PERFORM COMPARISON OF NEW SEQUENCE AND STORED SEQUENCE]
    210 --> 212{SAME?}
    212 -- YES --> 214[DISPLAY STORED SEQUENCE NAME TO USER]
    212 -- NO --> 218{MORE SEQUENCES IN DATABASE?}
    214 --> 218
    218 -- YES --> 224[GO TO NEXT SEQUENCE IN DATABASE]
    224 --> 210
    218 -- NO --> 220([END])
  
```

FIGURE. 2

100250-00755502

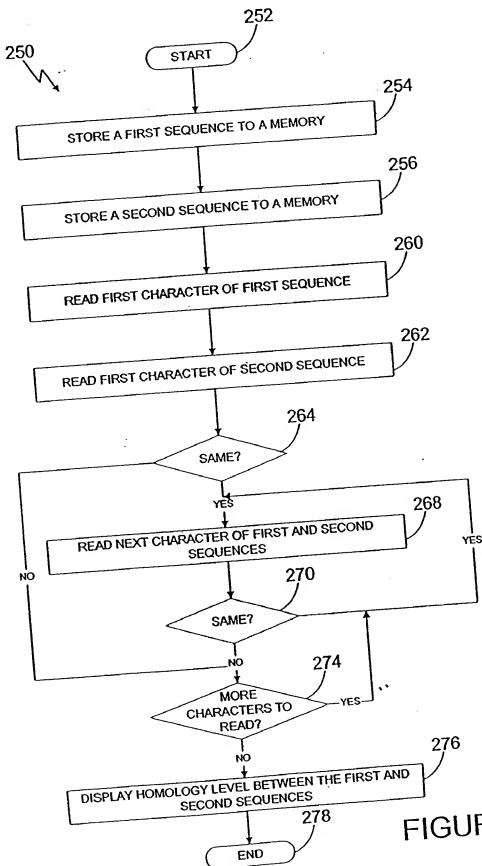


FIGURE 3

00000400-0000001

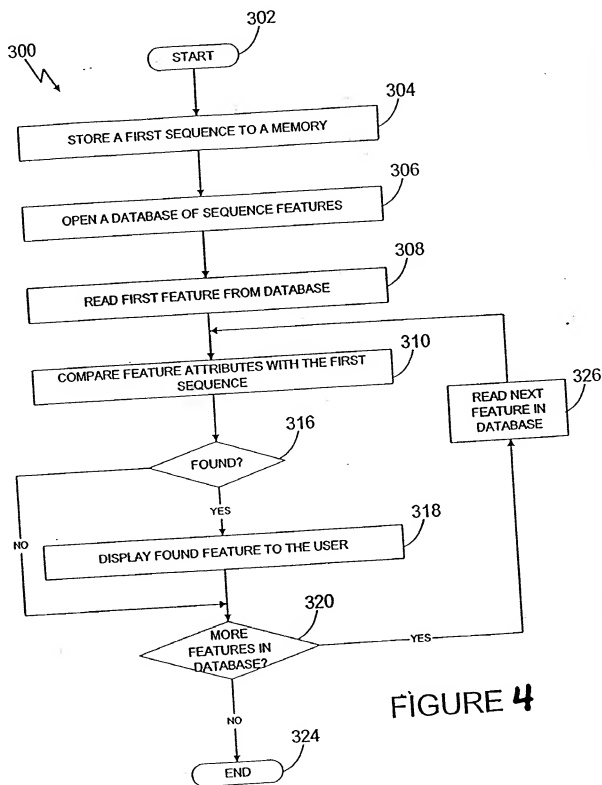


FIGURE 4

FIGURE 5

TTG AGA GCG CTC GTC TTT CAC GGC AAC CTC CAG TAT GCC GAA ATC CCA 48
 Leu Arg Ala Leu Val⁵ Phe His Gly Asn Leu¹⁰ Tyr Ala Glu Ile Pro¹⁵

AAG AGC GAA ATC CCA AAG GTC ATA GAG AAG GCA TAC ATC CCA GTC ATC 96
 Lys Ser Glu Ile²⁰ Pro Lys Val Ile Glu Lys Ala Tyr Ile Pro Val Ile³⁰

GAG ACA CTG ATT AAA GAA GAT CCT TTT GGG CTC AAC ATA ACG GGC 144
 Glu Thr Leu Ile³⁵ Lys Glu Glu Ile⁴⁰ Pro Phe Gly Leu Asn Ile Thr Gly⁴⁵

TAT ACC TTA AAG TTC CTC CCG AAG GAT ATT ATA GAC CTC GTT AAA GGG 192
 Tyr Thr Leu Lys Phe Leu⁵⁰ Pro Lys Asp Ile⁵⁵ Ile Asp Leu Val Lys Gly⁶⁰

GGC ATC GCG AGT GAC CTG ATA GAG ATA ATC GGA ACG AGC TAC ACG CAC 240
 Gly Ile Ala Ser Asp Leu⁶⁵ Ile Glu Ile Ile⁷⁰ Gly Thr Ser Tyr Thr His⁸⁰

GCA ATA CTC CCC CTC CTC CCG CTT AGC AGA GTA GAA GCA CAA GTT CAG 288
 Ala Ile Leu Pro⁸⁵ Leu Leu Pro Leu Ser Arg Val Glu Ala Gln Val Gln⁹⁵

AGA GAT AGG GAA GTT AAG GAA GAG CTC TTC GAG CTT TCT CCA AAG GGA 336
 Arg Asp Arg Glu Val¹⁰⁰ Lys Glu Leu Phe Glu Val Ser¹¹⁰ Pro Lys Gly¹¹⁵

TTC TGG CTG CCA GAG CTC GCC TAT GAC CCG ATA ATC CCT GCC ATA CTG 384
 Phe Trp Leu Pro Glu Leu Ala¹²⁰ Tyr Asp Pro Ile Ile¹²⁵ Pro Ala Ile Leu¹³⁰